

Figure 1. Single-crossover recombination.

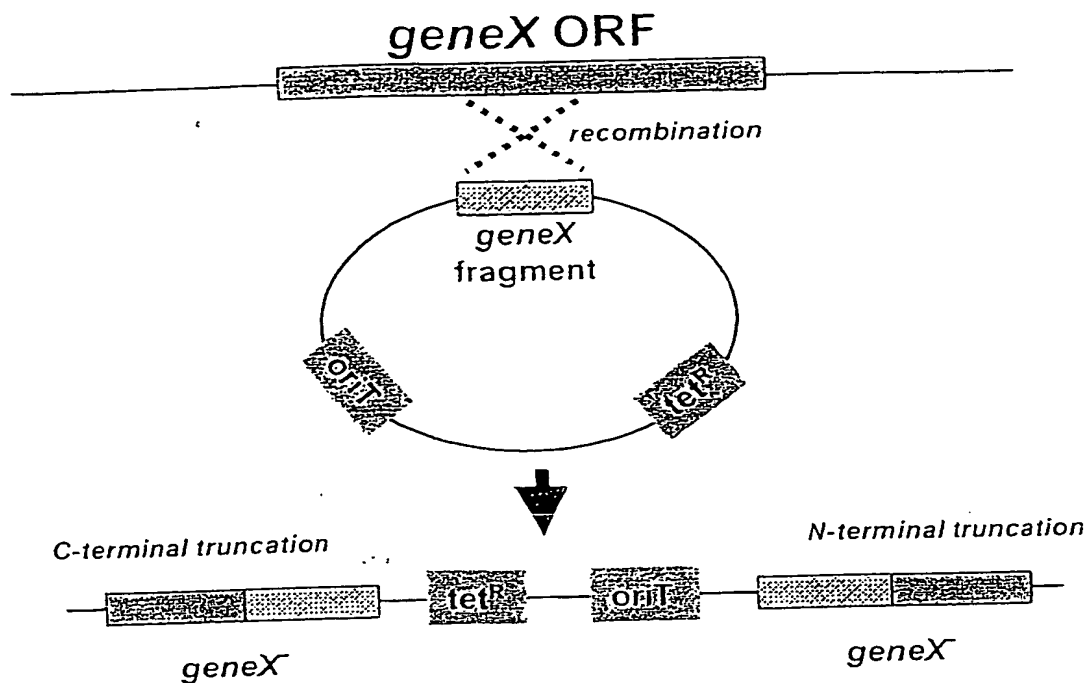
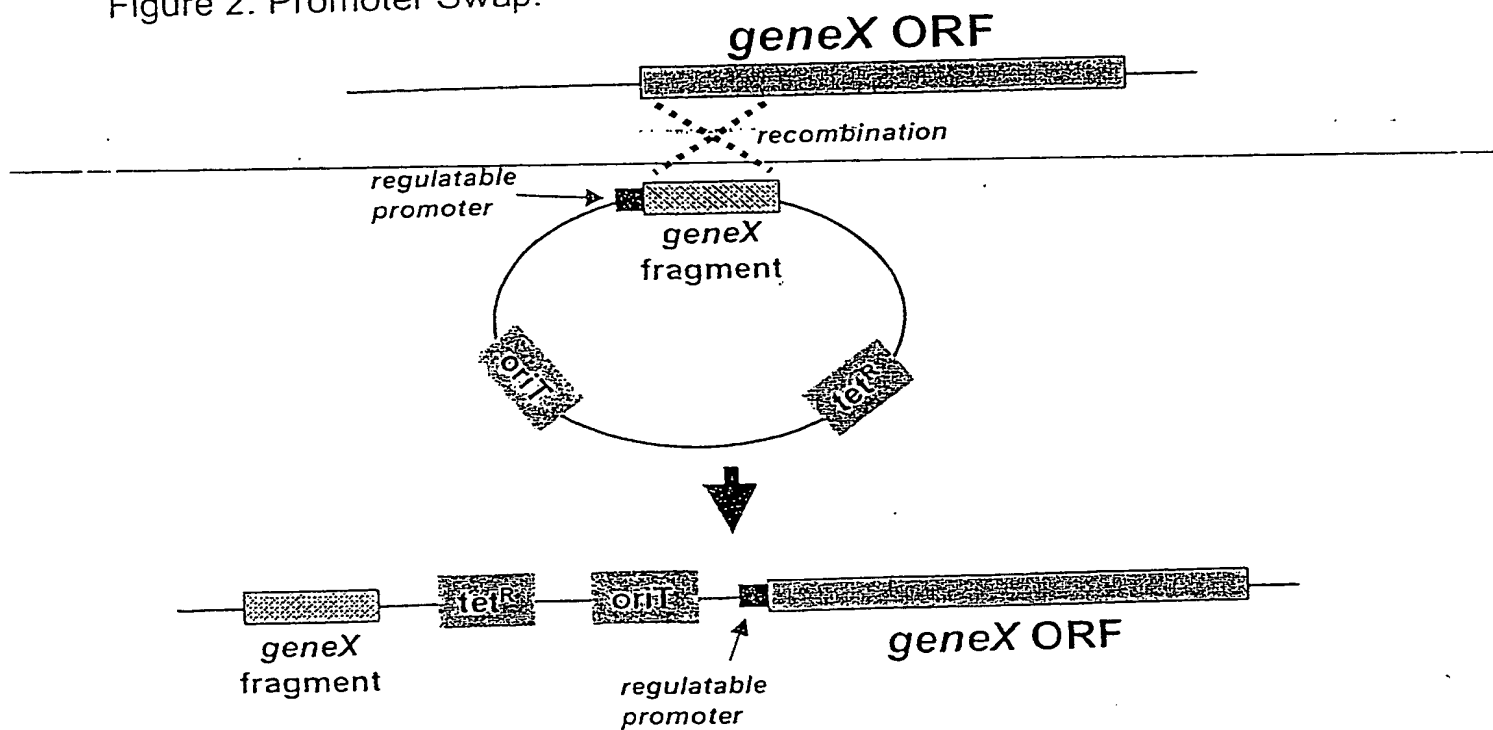


Figure 2. Promoter Swap.



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pMOD

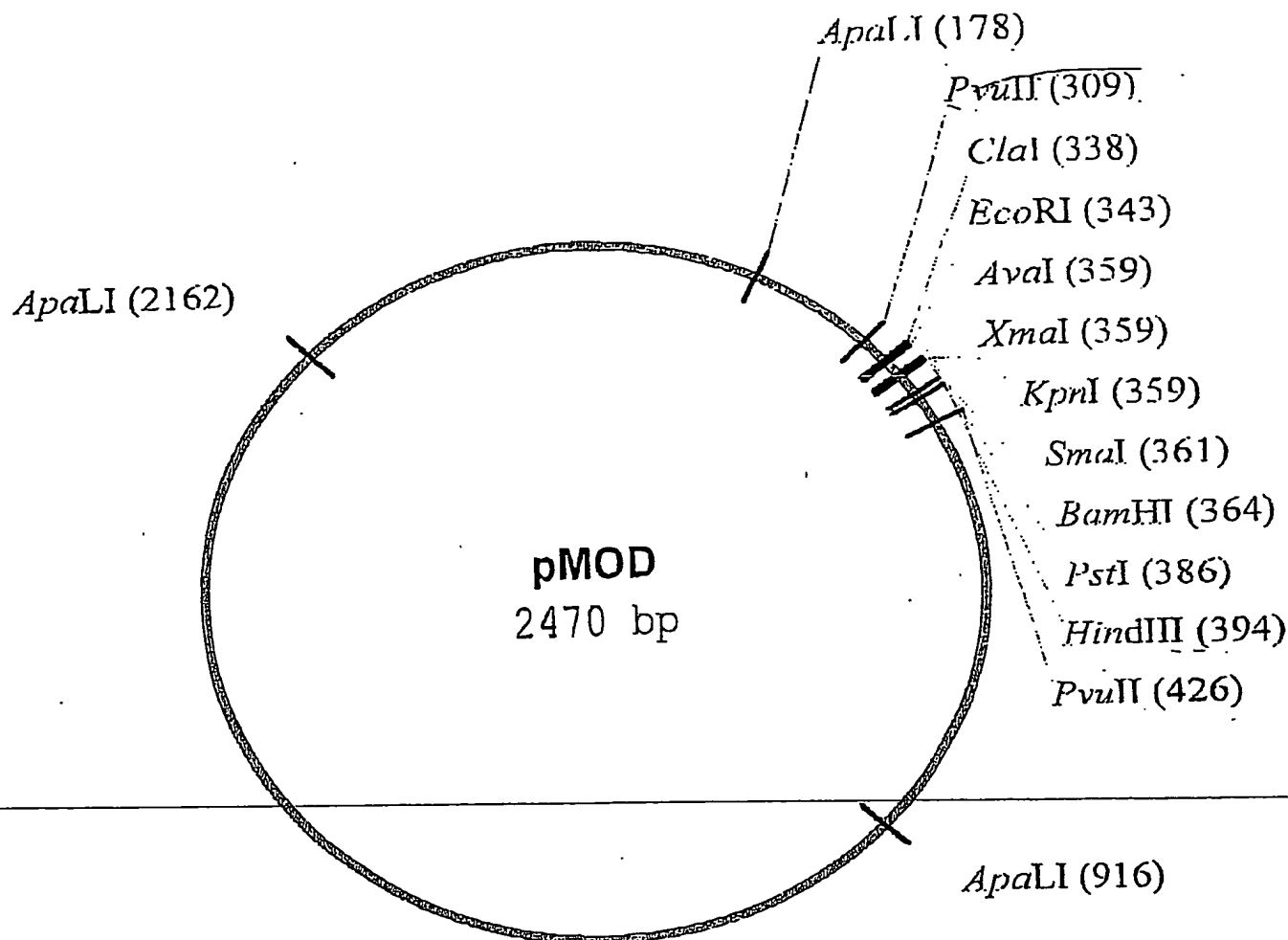


FIGURE 3

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pMOD (Erm-1)

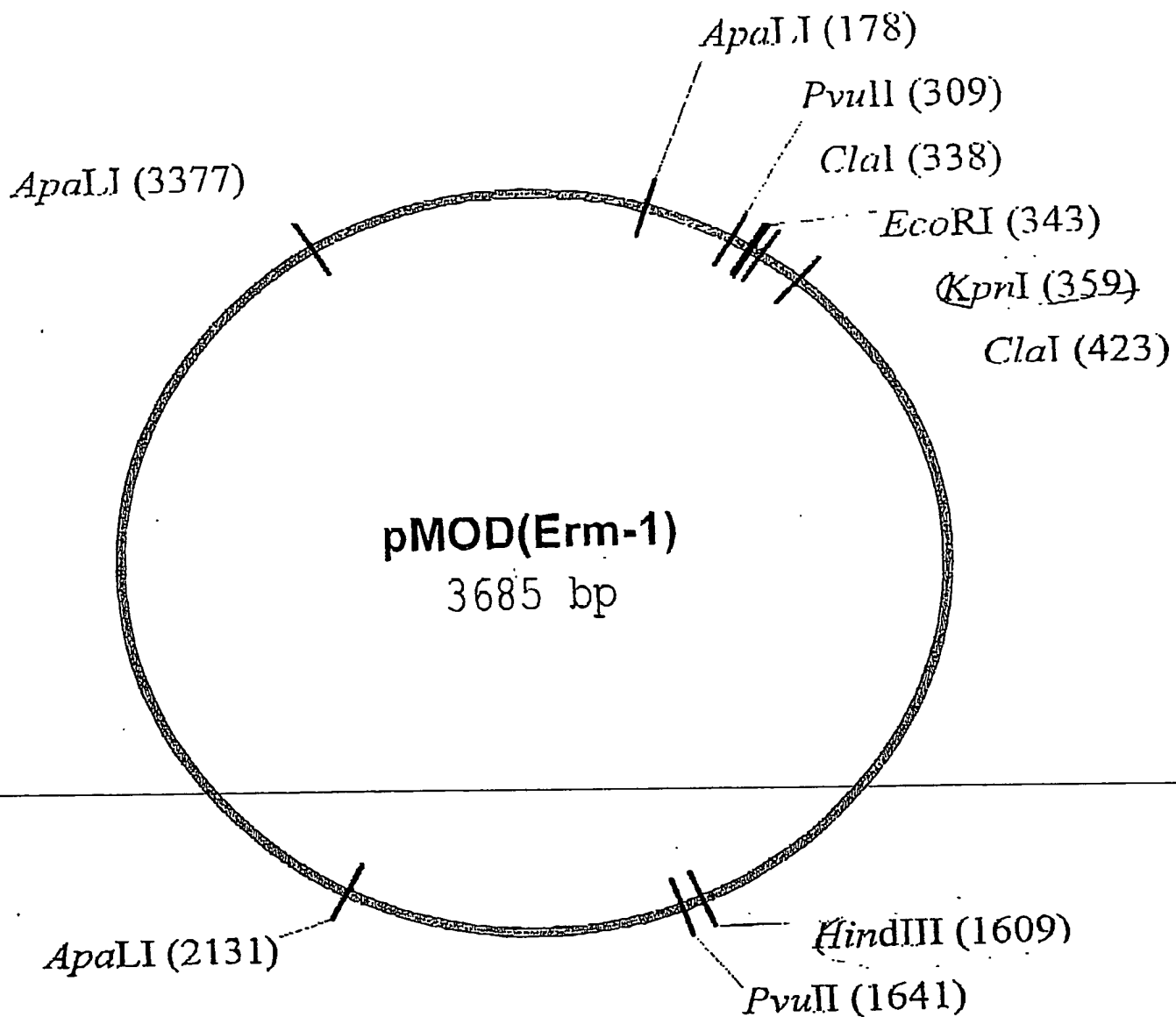
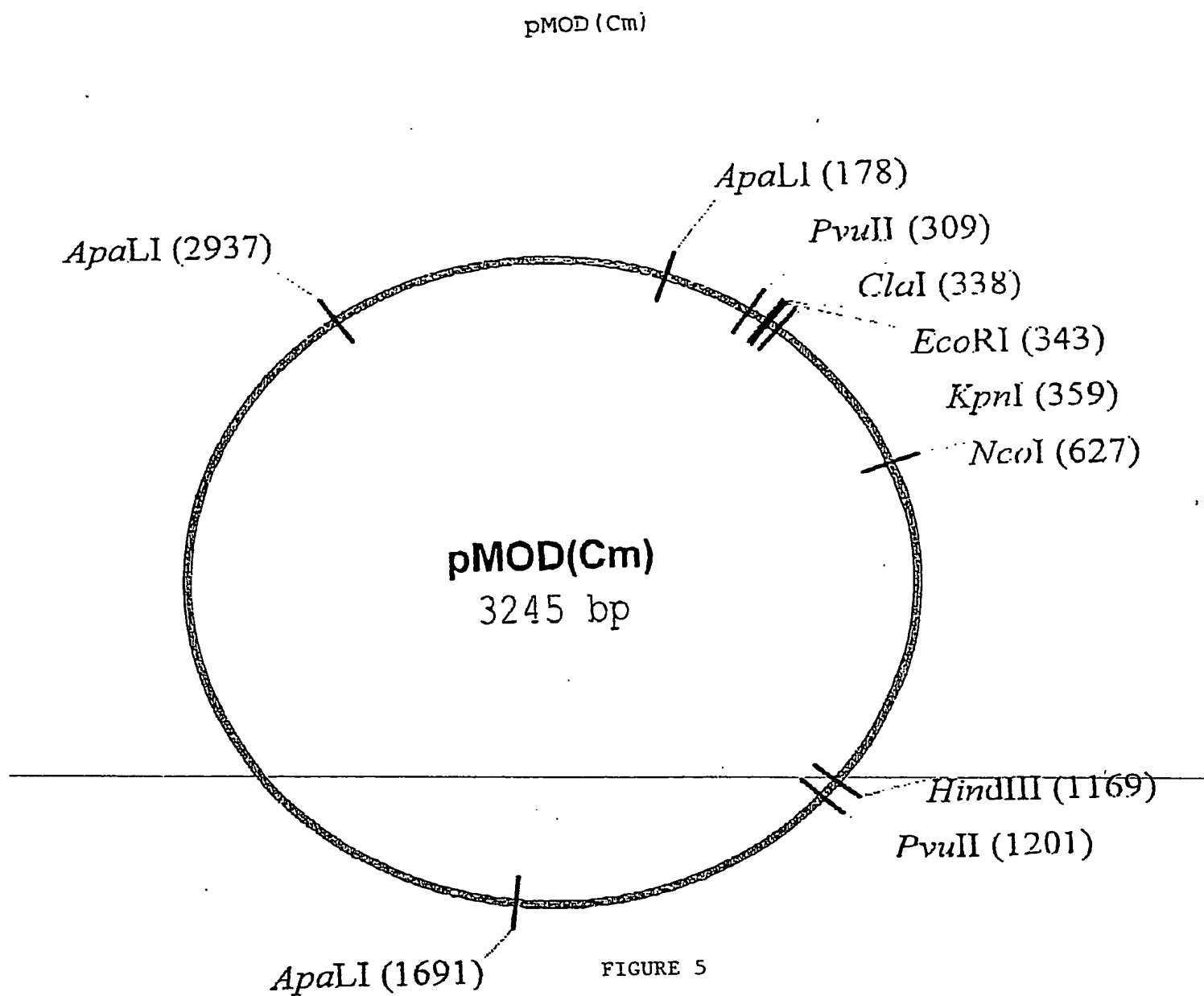


FIGURE 4



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FIGURE 6

pMOD

1 TCGCGCGTTT CGGTGATGAC GGTGAAAACC TGTGACACAT GCAGCTCCCG
 AGUGCGCAAA GCCACTACTG CCACTTTTGG AGACTGIGTA CGTCGACCGC
 51 GAGACGGTCA CAGCTTCTCT GTAAGGGAT GUGUGGAGCA GACAAGCGCG
 CTCTGCCAGT GTCGAACACA CATTGCGCTA CGCCCTTGGT CTGTTGGGGC
 101 TCAGGGCGCG TCAGCGGGTG TTGGCGGGTG TCGGCGCTGG CTTAAGTATG
 AGTCCCGCGC AGTCGCCCCAC AACCGCCAC AGCCCCGACC GAATTGATAC
 ApaLI
 151 CGGCATCAGA GCAGATTGTA CTGAGAGTGC ACCATATGCG GTGTGAAATA
 GCCGTAGTCT CGTCTAACAT GACTCTCAGG TGGTATACCG CACAUTTTAT
 201 CCGCACAGAT GCGTAAGGAG AAAATACCGC ATCAGCGCGC ATTGGCCATT
 GCGGTGTCTA CGCATTCCTC TTTTATGGCG TAGTCCCGCG TAAGCGGTAA
 251 CAGCCTGCGC AACTGTTGGG AAGGGCGATC GGTGCGGGCC TCTTGGCTAT
 GTCGACGCG TTGACAACCC TTCCCGCTAG CAGCGCGCG AGAAGCGATA
 EcoRI
 301 TACGCCAGCT GTCTCTTATA CACATCTCPA CCATCATCGA TCAATTCGAG
 ATGCGGTCTGA CAGAGAAATAT GTGTAGAGTT GGTAGTAGCT ACTTAAGCTC
 KpnI BamHI
 351 CTCGCTACCC GGGGATCCTC TAGAGTCGAC CTCCAGGCAT GCAAGCTTCA
 GAGCCATGGG CCGCTAGGAG ATCTCAGCTG CACGTCCGTA CGTTCGAAGT
 SmaI XmaI Aval
 401 GGGTTGAGAT CTGTATPAGA GACAGCTGCA TTAATGAATC GGCACGCGG
 CCCAACTCTA CACATATTCT CTGTGACGT AATTACTTAG CCGGTTGCGC
 451 CCGGGAGAGG CGGTTTGGCT ATTGCCCCCT CTTCGGCTTC CTCGCTCACT
 GCCCCCTCC GCCAAACGCA TAACCCGCCA GAAGCGGAAG GAGCGACTCA
 501 GACTCGCTGC GCTCGGTCTG TCGGCTGCGG CGAGUGGTAT CAGCTCACTC
 CTGAGCGACG CGAGCCAGCA AGCGGACGCC GCTCGCCATA GTCEAGTEAG
 551 AAAGGCGGTA ATACGGTTAT CCACAGAATC AGGGGATAAC GCAGGAAAGA
 TTTCCGCCAT TATGCCAATA GGTGTCTTAG TCCCTATTG CGTCCTTTCT
 601 ACATGTGAGC AAAAGGCCAG CAAAGGCCA GGAACCGTAA AAAGGCCGCG
 TGTACACTCG TTTTCCGGTC GTTTTCCGGT CTTGGCATT TTTCCGGCGC
 651 TTGCTGGCGT TTTTCCATAG GCTCCGCCCC CTTGACGAGC ATCACAAAA
 AACGACCGCA AAAAGGTATC CGAGGCGGGG GGAAGTCTCG TAGTGTTTTT
 701 TCGACGCTCA AGTCAGAGGT GGCGAAACCC GACAGGACTA TAAAGATACC
 AGCTGCGAGT TCAGTCTCCA CCGCTTTGGG CTGTCTGAT ATTTCTATCC
 751 AGGCGTTTCC CCGTGAAGC TCCCTCGTGC GCTCTCTGT TCCGACCTTG
 TCCGCAAAGG GGGACCTTCG AGGGAGCAGC CGAGAGGACA AGGCTGGGAC
 801 CCGCTTACCG GATACCTGTC CGCCTTTCTC CTTCCGGGAA GCGTGGCGCT
 GCGGAATGGC CTATGCACAG GCGGAAAGAG GGAAGCCCTT CGCACCGGCA
 851 TTCTCATAGC TCACGCTGTA GGTATCTCAG TTCGGTGTAG GTCGTTCCCT
 AAGAGTATCG AGTGGGACAT CCATAGAGTC AAGCCACATC CAGCAAGCGA
 ApaLI
 901 CCAAGCTGGG CTGTGTGCAC GAACCCCCCG TTCAGCCCGA CUGCTGCGCC
 GGTTCGACCC GACACACGTG CTTGGGGCCC AAGTCGGGCT GGCGACGCGG

pMOD

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951  TTATCCGCTA ACTATCGTCT TGATTCCTAC CCGCTAAGAC AGGACTTATC
    AATAAGCCAT TGATAGCAGA ACTCAGGTTG GGCCATTCTG TGCTGAATAG
1001  GGCCTGCGCA GCACCCACTG GTAACAGGAT TACCAGAGCG AGGTATGTAC
    CGCTGACCGT CGTCGGTGAC CATTTGCTTA ATCGTCTCGC TCCATACATC
1051  GCGGTGCTAC ACAGTTCTTG AAGTGGTGGC CTAACACGG CTACACTAGA
    CGCCACGATG TCTCAACAAC TTCACCACCG CATTGATGCC GATGTGATCT
1101  AGGACAGTAT TTGGTATCTG CGTCTGCTG AAGCCAGTTA CCTTCCCAAA
    TCGTGTCTTA AACCATAGAC GCGAGACGAC TTCGGTCAAT GGAAGCCTTT
1151  AAGAGTTCTG AGCTCTTGAT CCGGCAACA AACCAACGCT GGTAGCGCTG
    TTCTCAACCA TCGAGAATA GGCCGTTTGT TTGCTGGCGA CCATCGCCAC
1201  GTTTTTTTGT TTGCAAGCAG CAGATTACGC CCAGAAAAAA AGGATCTCAA
    CAAAAAACA AACGTTCTG GTCTAATGCG CGTCTTTTTT TCCTAGAGTT
1251  GAAGATCCTT TGATCTTTTC TACGGGGTCT GACGCTCAGT GGAACGAAAA
    CTCTAGGAA ACTAGAAAAG ATGCCCCAGA CTGCGAGTCA CTTTGGTTTT
1301  CTCAGGTTAA GGGATTTTGC TCATGAGATT ATCAAAAGG ATCTTCACTT
    GAGTGCAATT CCTAAAACC AGTACTCTAA TAGTTTTTCC TAGAAGTGG
1351  AGATCCTTTT AAATTAAAA TGAAGTTTTA AATCAATCTA AAGTATATAT
    TCTAGGAAAA TTAAATTTTT ACTTCAAAAT TTAGTTAGAT TTCATATATA
1401  GAGTAACTT GGTCTGACAG TTACCAATGC TTAATCAGTG AGGCACCTAT
    CTCATTTCAA CCAGACTGTC AATGGTTACG AATTAGTCA TCGGTGGATA
1451  CTCAGCGATC TGCTATTTTC GTTCATCCAT AGTTGGCTGA CTCCCCCTCG
    GAGTCGCTAG ACAGATAAAG CAAGTAGGTA TCAACGGACT GAGGGCCAGC
1501  TGTAGATAAC TACGATACGG GAGGGCTTAC CATCTGGCCC CAGTGTCTGA
    ACATCTATTG ATGCTATGCC CTCCCGAATG GTAGACGGG GTCACGAGCT
1551  ATGATACCGC GAGACCCACG CTCACCGGCT CCAGATTTAT CAGCAATAAA
    TACTATGGCG CTCTCGGTGC GAGTGGCCCA GGTCTAAATA GTCGTTATTT
1601  CCAGCCAGCC GGAAGGGCCG AGCGCAGAAG TGGTCTCTCA ACTTTATCCG
    GGTGCGTGG CCTTCCCGGC TCGCTCTTC ACCAGGACGT TCATATAGGC
1651  CCTCCATCCA GTCTATTAAT TGTGCCCCG AAGCTAGAGT AAGTAGTTCC
    GGACCTAGGT CAGATAATTA ACAACGGCCC TTCGATCTCA TTCATCAAGC
1701  CCAGTTAATA GTTTGCGCAA CGTTGTGCCC ATTGCTACAG CCATCGTGGT
    GGTCAATTAT CAAACGCGT GCAACAACGG TAACGATGTC CGTAGCACCA
1751  GTCACGCTCG TCGTTTGGTA TGGCTTCATT CAGCTCCGGT TCCCAACGAT
    CAGTCCGAGC AGCAAACCAT ACCGAAGTAA GTGAGGCCA AGGGTTGCTA
1801  CAAGGCGAGT TACATGATCC CCCATGTTCT GCAAAAAACC GGTAGCTCC
    GTTCCGCTCA ATGACTAGG GGGTACAACA CGTTTTTTCC CCAATCGAGG
1851  TTCGGTCTTC CGATCGTTGT CAGAAGTAAG TTGGCCGCAC TGTATCACT
    AAGCCAGGAG GCTAGCAACA GTTTTCATTC AACCGCGCTC ACAATAGTGA
1901  CATGETTATG GCAGCACTGC ATAATTCTCT TACTGTCTAG CCATCCGTAA
    GTACCAATAC CGTCGTGACG TATTAAGAGA ATGACAGTAC GGTAGGCATT
1951  GATGCTTTTC TGTGACTGGT GAGTACTCAA CCAAGTCATT CTGAGAATAG
    CTACGAAAAG AACTGACCA CTCATGAGT CGTTCAGTAA GACTCTTATC
2001  TGTATCGGCG GACCGAGTTC CTCCTGCCCC GCGTCAATAC GGGATAATAC
    ACATACGCCC CTGGCTCAAC CAGAACGGGC CGCAGTTATG CCTATTATG
2051  CGCGCCACAT AGCAGAACTT TAAAGTGCT CATCATTTGA AACGTTCTT
    GCGCGGTGTA TCGTCTTGAA ATTTTCACGA GTAGTAACCT TTTGCAAGAA
2101  CGGGGCGAAA ACTCTCAAGG ATCTTACCGC TGTGAGATC CAGTTCGATG
    GCGCGCTTT TGAGAGTTCC TAGAATGGCG ACAACTCTAG GTCAAGCTAC

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PMOD

ApalI
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|      |             |            |            |            |             |
|------|-------------|------------|------------|------------|-------------|
| 2151 | TPACCCACTC  | GTGCACCCAA | CTGATCTTCA | GCATCTTTTA | CTTTCACCAAC |
|      | ATTGGGGTGAG | CAUGTGGGGT | GACTAGAAAT | CGTAGAAAT  | GAAAGTGGTC  |
| 2201 | CGTTTCTGCC  | TGAGCAAAAA | CAGCAAGGCA | AAATGCCGCA | AAAAAGGGAA  |
|      | GCAAGAGCCC  | ACTCGTTTTT | GTCCTTCCGT | TTTACGGCGT | TTTTTCCCTT  |
| 2251 | TAAGGGCGAC  | ACGGAAATGT | TGAATACTCA | TACTCTTCCT | TTTTCAATAT  |
|      | ATTCCCGCTG  | TCCCTTTACA | ACTTATGAGT | ATGAGAAACA | AAAAGTTATA  |
| 2301 | TATTGAAGCA  | TTTATCAGGG | TTATTGTCTC | ATGAGCGGAT | ACATATTTGA  |
|      | ATAACTTCGT  | AAATACTCCC | ATAACAGAG  | TACTCGCCTA | TGTATAAACT  |
| 2351 | ATGTATTTAG  | AAAAATAAAC | AAATAGCGCT | TCCGCGCACA | TTTCCCCGAA  |
|      | TACATAAATC  | TTTTTATTTG | TTTATCCCCA | AGGCGCGTGT | AAAGGCGCTT  |
| 2401 | AAGTCCCACC  | TGACGTCTAA | GAAACCATTA | TTATCATGAC | ATTAACCTAT  |
|      | TTCACGCTGG  | ACTGCAGATT | CTTTGGTAAT | AATAGTACTG | TAATTGGATA  |
| 2451 | AAAATAGGC   | GTATCACCAG |            |            |             |
|      | TTTTTATCCG  | CATAGTGCTC |            |            |             |

FIGURE 7

pMOD (E1M-1)

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1  TCGCGCGTTT CCTGATGAC GGTCAAAACC TCTGACACAT GCAGCTCCCG
   AGCGCGCAA GCCACTACTG CCACPTTTGG AGACTGTGTA CGTGAGGGG
51  GAGACCGTCA CAGCTTGTCT GTAAGCGGAT GCCCGGAGCA GACAAACCCG
   CTCTGCCAGT GTGGAACAGA CATTGCGCTA CGGCCCTCGT CTGTTTGGCC
101 TCAGCGCGCG TCAGCGUETE TTGGCGGCTG TCGGAGCTGG CTTAACTATG
   AGTCCCGCGC AGTCGCCCCAC AACCGCCCA AGCCCGGACC GAATTGATAC
                                     ApaLI
151 CGGCATCAGA GCAGATTGTA CTGAGAGTGC ACCATATGCG GTGTGAAATA
   CCGGTAGTCT CGTCTAACAT GACTCTCAG TGGTATACCC CACACTTTAT
201 CCGCACAGAT GCGTAAGGAC AAAATACCGC ATCAGGCGCC ATTGCGCAT
   GCGGTGTCTA CGCATTCCTC TTTTATGGCG TAGTCCGCGG TAAGCGGTAA
251 CAGGCTGCGC AACTGTTGGG AAGGGCGATC GGTGCGGGCC TCTTGGGTAT
   CTCGACGCGG TTGACAACCC TTCCCGCTAC CCACGCGCGG ACAAGCGATA
                                     EcoRI
301 TACGCCAGCT CTCTCTTATA CACATCTCAA CCATCATCGA TGAATTGAG
   ATCGGGTCGA CAGAGAATAT GTGTAGAGTT GGTAGTAGCT ACTTAAGCTC
                                     PvuII
351 CTCGGTACCG TACCATTCAA ATTTATCCTT ATTGTACAAA ATAACAGCGA
   CAGCCATGGC ATGGTAAGTT TAAATAGGAA TAACATGTTT TATTGTGCGT
                                     KpnI
401 AATTTTTTAA TCTATTCCTT ATCCATACAA ATTCCCGGTA GCGGCTAGGG
   TTAATAATTT AGATAAGGAA TAGCTATGTT TAAGGGGCGAT CCGCGATCCG
451 ACCTCTTTAG CTCCTTGGA GCTGTGAGTA GTATACCTAA TAATTTATCT
   TGGACAAATC GAGGAACCTT CGACAGTCAT CATATGGATT ATTAATAGA
501 ACATTCCCTT TACTAACGTG TAACCTTCCA AATTTACAAA AGCGACTCAT
   TGTAAAGGAA ATCATTGCAC ATTGAAGGTT TAAATGTTT TCGCTGAGTA
551 AGAATTATTT CCTCCCGTTA AATAATAGAT AACTATTAAA ATAGACAAAT
   TCTTAATAAA GGAGGGCAAT TTATTATCTA TTGATAATTT TTATCTGTTA
601 ACTTGCTCAT AATAACGGT ACTTAAATTG TTTACTTTCG CGTGTTCAT
   TGAACGAGTA TTCATTGCCA TGAATTTAAC AAATGAABCC GCACAAAGTA
651 TGCTTGAGAA ACTGATTTT AGTAACAGT TGAUGATATT CTCGATTGAC
   ACGAACACTT TGAATAAAA TCATTGTCA ACTGCTATAA GAGCTAACTG
701 CCATTTTGAA ACAAAGTACG TATATAGCTT CCAATATTTA TCTGGAACAT
   GGTAAAACTT TGTTTCATGC ATATATCGAA GCTTATAAAT AGACCTTETA
751 CTGTGCTATG GCGGGTAAGT TTTATTAAGA CACTGTTTAC TTTTGGTTTA
   GACACCATAC CGCCCATTC AATAATTTCT GTGACAAATG AAAACCAAAT
801 CGATGAAAGC ATTCCGCTGG CAGCTTAAGC AATTGCTGAA TCGAGACTTG
   CCTACTTTTCG TAAGGCGACC GTCGAATTCG TTAACGACTT AGCTCTGAAC
851 AGTGTGCAAG AGCAACCTA GTGTTGCGTG AATATCCAAG CTACGCTTGT
   TCACACGTTT TCGTTGGGAT CACAAGCCAC TTATAGGTTT CATGCGAACA
901 AGAATCCTTC TTCAACAATC AGATAGATGT CAGACGCATG GCTTTCAAAA
   TCTTAGGAAG AAGTTGTTAG TCTATCTACA GTCTGCGTAC CGAAAGTTTT
951 ACCACTTTTT TAATAATTTG TGTGCTTAAA TGGTAAGGAA TATTCCCAAC
   TGGTGAAAAA ATTATTAAC ACACGAATTT ACCATTCTTT ATAAGGGTTG
1001 AATTTTATAC CTCTGTTTGT TAGGGAATTG AACTGTAGA ATATCTTGGT
   TTAAATATG GAGACAAACA ATCCCTTAAC TTTGACATCT TATAGAACCA

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pMOE (EX-1)

1051 GAAATTAAGT GACACGAATG TTCAGTCTTA ATTTTCTCGA CGATAACTTG  
 CTTAATTTCA CTGTCTTAC AAGTCAAAAT TAAAAAGSC GCTATTCAAC  
 1102 AATAGATGAC TGTCTAATTC AATAGACCTT ACCTGTTTAC TTATTTTAGC  
 TTATCTACTG ACAGATTAGG TTATCTGCAA TGGACAAATG AATAAAATCG  
 1151 CAGTTTCCTC GTTAAATGCC CTTACCTGT TCCAATTTCT TAAACGGTAT  
 GTCAAAGCAG CAATTTACGG GAAATGGACA AGETTAAAGC ATTTGCCATA  
 1201 CGGTTTCTTT TAAATTCAAT TGTTTTATTA TTTGGTTGAG TACCTTTTCA  
 GCCAAAGAAA ATTTAAGTTA ACAAAATAAT AAACCAACTC ATGGAAAAGT  
 1251 TTCGTTAAAA AGTTTGGAGA ATATTTTATA TTTTGTTC TCTAATCACT  
 AAGCAATTTT TCAAACTCT TATAAATAI AAAACAAGT ACATTACTGA  
 1301 CCTGAAGTGA TACATCTATA AATAAATACA GAAGTTAAAC GATTGTTTTG  
 CGACTTCACT ATCTAGATAT TTATTTATGT CTCAATTTG CTAACCAAC  
 1351 TAATTTTAST TATCTGTTA AAAAGTCATA AGATTAGTCA CTGGTAGGAA  
 ATTAATAATCA ATAGACAAAT TTTTCAGTAT TCTAATCAGT GACCATCCTT  
 1401 TTAATCTAAA CGTATTTATC TGCGTAATCA CTGTTTTTAG TCTGTTTCAA  
 AATTAGATTT GCATAAATAG ACGCATTAGT GACAAAAATC AGACAAAGTT  
 1451 AACAGTAGAT GTTTTATCTA CATTACGCAT TTGGARTACC AACATGACGA  
 TTGTCATCTA CAAAATAGAT CTATGCGTA AACCTTATGG TTGTACTGCT  
 1501 ATCCCTCCTT CTTAATTACA AATTTTTAGC ATCTAATTTA ACTTCAATTC  
 TAGGGAGGAA GAATTAATGT TTAATAATCG TACATTAAAT TGAAGTTAAG  
 1551 CTATTATACA AAATTTTAAG ATAATGCACT ATCAACACAC TCTTAAGTTT  
 GATAATATGT TTAATAATTC TATTACCTGA TAGTTGTGTG AGAATTCAA  
  
 HindIII PvuII  
 1601 GCTTCTAAG CTTCAGGGTT GAGATGTCTA TAAGAGACAC CTGCATTAAT  
 CGAAGATTTT GAAGTCCCAA CTCTACACAT ATTCTCTGTC GAGGTAATTA  
 1651 GAATCGGCGA ACGCGCGGGG AGAGGCGGTT TCGGTATTGG GCGCTCTTCC  
 CTTACCCGCT TCGGCGCGCC TCTCGCCTAA ACGCATAACC CCGCAGAAGG  
 1701 GCTTCTCGC TCACTGACTC GCTGCGCTCG GTCGTTCGGC TCGGGCGAGC  
 CCAAGGAGCG AGTGACTGAG CCACGCGAGC CAGCAAGCCG ACGCCGCTCG  
 1751 CGTATCAGCT CACTCAAAGG CGGTAAATCG GTTATCCACA GAATCAGGGG  
 CCATAGTCGA GTGAGTTTCC GCCATTATGC CAATAGGTGT CTTAGTCCCC  
 1801 ATAACGCAGG AAAGAACATG TGAGCAAAAG GCCAGCAAAA GGCCAGGAAC  
 TATTGCGTCC TTTCTGTGAC ACTCGTTTTC CGGTCGTTT CCGGTCCTTG  
 1851 CGTAAAAAGG CCGCGTTGCT GCGTTTTTTC CATAGGCTCC GCGCCCTTGA  
 GCATTTTTC GCGCAACGA CCGCAAAAG GATCCGAGG GCGGGGAGT  
 1901 CCAGCATCAC AAAAATCGAC GCTCAAGTCA GAGGTGGCGA AACCCGACAG  
 GCTCGTAGTG TTTTAGCTG CGAGTTTCACT CTCCACCGCT TCGGCTGTC  
 1951 GACTATAAAG ATACCAGGCG TTTCCCTCTG GAAGCTCCCT CGTGCCTCT  
 CTGATATTTT TATGGTCCGC AAAGGGGGAC CTTGAGGGA GCACGCGAGA  
 2001 CCTGTTCCGA CCTGCGGCT TACCGGATAC CTGTCCGCTT TTCTCCCTTC  
 GGACAAGGCT GGGACGGCGA ATGGCCTATG GACAGCGGGA AAGAGGGGAG  
 2051 GGGAGCGGTG GCGCTTTCTC ATAGCTCAUG CTGTAGGTAT CTCAGTTCGG  
 CCTTCCAC CCGGAAGAG TATCGAGTGC GACATCCATA GAGTCAAGCC  
  
 ApaI  
 2101 TGTAGGTCGT TCGCTCCAAG CTGGGCTGTG TGCACGAACC CCGGTTCCAG  
 ACATCCAGCA ACGGAGGTTT GACCCGACAC ACGTGCTTGG GGGGCAAGTC  
 2151 CCGGACCGCT GCGCCTTATC CGGTAAGTAT CGTCTTGAGT CCAACCCGCT  
 GGGCTGGCGA CCGGAATAG GCCATTGATA GCAGAACTCA GGTGGGCCA

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pMOD (Erm-1)

2201 AAGAACGGAC TTATCGCCAC TGGCAGCAGC CACTGGTAAC AGGATTAGCA  
TTCTGTGCTG AATAGCGGTG ACCGTCGTCC CTGACCATTG TCCTAATCGT  
2251 GACCGAGGTA TGTAGGCGGT GTTACAGAGT TCTTGAAGTG GTGGCCTAAC  
CTCCCTCCAT ACATCCGCCA CCATGTCTCA AGAACCTTCA CACCGGATTG  
2301 TACGGCTACA CTAGAAGGAC AGTATTTGGT ATCTCCGCTC TGCTGAAGCC  
ATGCCGATGT GATCTTCCTG TCATAAACCA TAGACCGGAG ACGACTTCGG  
2351 AGTTACCTTC GGAAAAAGAG TTGGTAGCTC TTGATCCGGC AAACAAACCA  
TCATGCGAAG CCTTTTCTC AACCATCGAG AACTAGGCCG TTTGTTGGT  
2401 CCGCTGGTAG CGGTGGTTTT TTGTTTTCCA AGCAGCAGAT TACGCGCAGA  
GGCGACCATC GCCACCAAA AAACAAAGCT TCGTCGTCTA ATGCGGCTCT  
2451 AAAAAGGAT CTCAAGAAGA TCCTTTGATC TTTTCTACGG GGTCTGACCC  
TTTTTTCTTA GAGTTCTTCT AGGAAACTAG AAAAGATGCC CCAGACTGCC  
2501 TCAGTCCAA C GAAACTCAC GTTAAGGGAT TTTGGTCATG AGATTATCAA  
AGTCACCTTG CTTTGTAGTG CAATTCCTTA AAACCAAGTAC TCTAATAGTT  
2551 AAAGGATCTT CACCTAGATC CTTTTAAATT AAAAATGAAG TTTTAAATCA  
TTTCCTAGAA GTGGATCTAG GAAAATTTAA TTTTACTTC AAAATTTAGT  
2601 ATCTAAAGTA TATATGAGTA AACTTGGTCT GACAGTTACC AATGCTTAA  
TAGATTTCAT ATATACTCAT TTGAACCAGA CTGTCAATGG TTACCAATTA  
2651 CAGTGAGGCA CCTATCTCAG CGATCTCTCT ATTTGCTTCA TCCATAGTTG  
GTCACTCCGT GGATACAGTC GCTAGACAGA TAAAGCAAGT AGGTATCAAC  
2701 CCTGACTCCU CGTCGTGTAG ATAACCTACG TACGCGAGGG CTTACCATCT  
GGACTGAGGG GCAGCACATC TATTGATGCT ATGCCCTCCC GAATGGTACA  
2751 GGCCCCAGTG CTGCAATGAT ACCGCGAGAC CCACGCTCAC CGGCTCCAGA  
CCGGGCTCAC GACGTTACTA TGGCGCTCTG GGTGCGAGTG GCGGAGGTCT  
2801 TTTATCAGCA ATAAACCAGC CACCCGGAAG GGCCGAGCGC AGAAGTGGTC  
AAATAGTCGT TATTGCTCG GTCCGCCCTC CCGGCTCGCG TCTTACCCAG  
2851 CTGGAAGTTT ATCCGCTTCC ATCCAGTCTA TTAATTGTTG CCGGGAAGCT  
GACGTTGAAA TAGGCGGAGG TAGGTGAGAT AATTAACAC CCGCCTTCGA  
2901 AGAGTAAGTA GTTCGCCAGT TAATAGTTTG CGCAACGTTG TTGCCATTGC  
TCTCATTCAT CAACCGGTCA ATTATCAAAC GCGTTGCAAC AACGGTAACG  
2951 TACAGGCATC GTGGTGTAC GCTCGTCGTT TGGTATGGCT TCATTGAGCT  
ATGTCCGTAG CACCACAGTG CGAGCAGCAA ACCATACCGA AGTAAGTCGA  
3001 CCGGTTCCCA ACGATCAAGG CGAGTACAT GATCCCCCAT GTTGTGCAAA  
GGCCAAGGGT TGCTAGTTCC GCTCAATGTA CTAGGGGGTA CAACACGTTT  
3051 AAAGCGGTTA GTCCTTCGC TCCTCCGATC GTTGTGAGAA GTAAGTTGGC  
TTTCGCCAAT CGAGGAAGCC AGGAGGCTAG CACAGTCTT CATTCACCCG  
3101 CGCAGTGTTA TCACTCATGG TTATGGCAGC ACTGCATAAT TCTCTTACTC  
GCGTCACAAT AGTGAGTACC AATACCGTCG TGACGTATTA AGAGAATGAC  
3151 TCATGCCATC CGTAAGATGC TTTTCTGTGA CTGGTGAGTA CTCAACCAAG  
AGTACGGTAG GCATTCTACG AAAAGACACT GACCACTCAT GAGTTGGTTC  
3201 TCATTCTGAG AATAGTGTAT GCGGCGACCG AGTTGCTCTT GCGGCGCTC  
AGTAAGACTC TTATCACATA CGCCGCTGGC TCAACGAGAA CCGGCCGAG  
3251 AATACGGCAT AATACGCGC CACATAGCAG AACTTTAAAA GTGCTCATCA  
TTATGCCCTA TTATGGCCG GTGTATCGTC TTGAATTTT CACGAGTAGT  
3301 TTGGAAAACG TTCTTCGGGG CGAAAACCTCT CAAGGATCTT ACCGCTGTTG  
AACCTTTTGC AAGAAGCCCC GCTTTTGAGA GTTCCTAGAA TGGCGACAC

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PMOD (ZEM-1)

Apal I

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3351 AGATCCAGTT CGATGTAACC CACTCGTGCA CCCAAGTGAT CTCAGGATC
      TCTAGGTCAA GCTACATTGG GTGAGCACGT GGGTTGACTA GAAGTCGTAG
3401 TTTTACTTTC ACCAGCGTTT CTGSGTGAGC AAAAACAGGA AGGCAAAATG
      AAAATCAAAG TGGTCGCAAA GAGGCACTCG TTTTGTCTT TCGGTTTTAC
3451 CCGCAAAAAA GGGAAATAAGG GCGACACGGA AATGTTGAAAT ACTCATACTC
      GGCCTTTTTT CCGTTATTCC CGCTGTCCCT TTACAACPTA TGAGTATCAG
3501 TTCCTTTTTT AATATTATTG AAGCATTTAT CAGGCTTATT GTCTCATGAC
      AAGGAAAAAG TTATAATAAC TTCTGTAATA GTUCCAATAA CAGAGTACTC
3551 CCGATACATA TTTGAATGTA TTTAGAAAAA TAAACAAATA GGGGTTCCGC
      GCTATGTAT AACTTACAT AAATCTTTTT ATTTCTTTAT CCCCAGGCG
3601 GCACATTTCC CCGAAAAGTG CCACCTGACG TCTAACAAAC CATTATTATC
      CGTGTAAGG GCGTTTTCAC GGTGGACTGC AGATTCTTTG GTAATAATAG
3651 ATGACATTAA CCTATAAAA TAGGGCTATC ACGAG
      TACTGTAATT GGATATTTTT ATCCGCATAG TGCTC
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pMOD (Cm)

FIGURE 8

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1  TCGCGGCTTT CGGTGATGAC GGTEAAAACC TGTGACACAT GCAGCTCCCG
   AGCGCGCAAA GCCACTACTC CCACTTTTUG AGACTGTETA CGTCGAGGCU
51  GAGACGOTCA CAGTTTGTCT GTAAGUGGAT GCCGGGAGCA GACAAGCCCC
   CTCTGCCAGT GTCGAACAGA CATTCCGCTA CGGCCCTCCT CTGTTCGGCC
101 TCAGGGCGCG TCACCGGGTG TTGCGGGGTG TCGGGGCTGG CTTAACTATE
   AGTCCCGCGC AGTCCCCCAC AACCGCCAC AGUCCGACC GAATTGATAC
                                     ApsI
151 CGGCATCAGA GCAGATTGTA CTGAGAGTGC ACCATATGCG GTGTGAAATA
   GCCGTAGTCT CGTCTAACAT GACTCTCAG TGGTATACGC CACACTTTAT
201 CCGCACAGAT CCGTAAGGAG AAAATACCGC ATCAGGCGCC ATTGCGCATT
   GCGGTGTCTA CCGATTCTTC TTTTATGGCG TAGTCCGCGG TAAGCGGTAR
251 CAGGCTGCGC AACTGTGGG AAGGGCGATC GGTGCGGCCC TCTTCGCTAT
   GTCCGACGCG TTGACAACCC TTCCCGCTAG CCACGCGCGG AGAAGCGATA
                                     EcoRI
                                     ClaI
301 TACGCCAGCT GTCTCTTATA CACATCTCAA CCATCATCGA TGAATTGAG
   ATCGCGTCCA CAGAGAATAT GTGTAGAGTT GGTAGTAGCT ACTTAAGCTC
                                     PvuII
351 CTCGGTACCG TTAGTGACAT TAGAAAACCG ACTGTAAAAA GTACAGTCCG
   GAGCCATGGC AATCACTGTA ATCTTTTGGC TGACATTTTT CATGTCACCC
401 CATTATCTCA TATTATAAAA GCCAGTCATT AGGCCTATCT GACAATTCCT
   GTAATAGAGT ATAATATTTT CGGTCAAGTA TCCGGATAGA CTGTTAAGGA
451 GAATAGAGTT CATAACAAT CTTGCATCAT AACCATCACA AACACAATGA
   CTTATCTCAA GTATTGTTA GGACGTACTA TTGTAGTCT TTGTCTTACT
501 TGTACCTGTA AAGATAGCGG TAAATATATT GAATTACCTT TATTAAAGAA
   ACATGGACAT TTCTATCGCC ATTTATATAA CTTAATGGAA ATAATTACTT
551 TTTCCCTGCT GTAATAATGG GTAGAAGGTA ATTACTATTA TTATGATAT
   AAAAGGACGA CATTATTACC CATCTTCCAT TAATGATAAT AATAACTATA
                                     NcoI
601 TTAAGTTAAA CCCAGTAAAT GAATCCATG GAATAATAGA AAGAGAAAA
   AATTCAATTT GGGTCATTTA CTTCAAGTAC CTTATTATCT TTCTCTTTT
651 GCATTTTCAG GTATAGGTGT TTTGGGAAAC AATTTCCCCG AACCATTATA
   CGTAAAGTC CATATCCACA AAACCTTTG TTAAGGGGC TTGGTAATA
701 TTTCTCTACA TCAGAAAGGT ATATATCATA AAACCTTTG AAGTCATTCT
   AAAGAGATGT AGTCTTTCCA TATTTAGTAT TTGAGAAAC TTCAGTAAGA
751 TTACAGCAGT CCAATACCA GAGAATGTT TAGATACACC ATCAAAATTT
   AATGTCCTCA GGTATATGGT CTCTTACAAA ATCTATGTGG TAGTTTTTA
801 GTATAAAGTG GCTCTAAGT ATCCCAATAA CCTAAGTCTC CGTCGCTATT
   CATATTTTAC CGAGATTGAA TAGGGTTATT GGATTGAGAG GCAGCGATAA
851 GTAACCAGTT CTAAAAGCTG TATTTGAGTT TATCACCCTT GTCATAACA
   CATTGGTCAA GATTTTCGAC ATAACTCAA ATAGTGGGAA CAGTGATTC
901 AAATAAATGC AGGGTAAAT TTATATCCTT CTTGTTTTAT GTTTCGGTAT
   TTTATTTACG TCCCATTTTA AATATAGGAA GAACAAAATA CAAAGCCATA
951 AAACACTAA TATCAATTTT TGTGGTTATA CTAAAAGTCG TTTGTTGGTT
   TTTTGTGATT ATAGTTAAG ACACCAATAT GATTTTCAGC AAACAACCAA
1001 CAAATAATGA TTAATATCT CTTTCTCTT CCAATTGCTT AATCAATTT
   GTTTATTACT AATTTATAGA GAAAGAGAA GGTAAACAGA TTTAGTTAAA

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EMOD (CPI)

|      | HindIII     |            |            |            | PvuII       |  |
|------|-------------|------------|------------|------------|-------------|--|
| 1051 | TATTAGAGTT  | CATTTGATAT | CCCTGCTAAA | TTTTTATATA | AAATGATTTA  |  |
|      | ATAATTTCAA  | GTAAACTATA | CCGAGGATTT | AAAAATAGAT | TTCACTTAAA  |  |
| 1101 | AGGAGGCTTA  | CTTGCTCTGT | TTCTTCATTA | CAATCAATCC | TTTTTAAAA   |  |
|      | TCTTCCGAAT  | GAACAGAUGA | AAGAACTAAT | CTTAGTTAGG | AAAAATTTT   |  |
| 1151 | GTCAATATTA  | CTGTAACAAG | CTTCAGGGTT | GAGATGTGTA | TAAGAGACAG  |  |
|      | CAGTTATAAT  | GACATTGTTC | GAAAGTCCCA | CTCTACACAT | ATTCTCTGTC  |  |
| 1201 | CTGCATTAAT  | GAATCGGCCA | ACGUGCGGGG | AGAGGCCGTT | TGCGTATTGG  |  |
|      | GACGTAATTA  | CTTAGCCGGT | TGUGUGCCCC | TCTCCGCCAA | ACGCATAACC  |  |
| 1251 | CGGCTCTTCC  | CCTTCCTCGC | TCACTGACTC | GCTGCGCTCG | GTGCTTCGGC  |  |
|      | CGCGAGAAAG  | CCAAGGAGCG | AGTGACTGAG | CGACGCGAGC | CAGCAAGCCG  |  |
| 1301 | TGCGGCGAGC  | GGTATCAGCT | CACTCAAAGG | CGGTAATACG | GTTATCCACA  |  |
|      | ACGCGCGCTCG | CCATAGTCCA | GTGAGTTTCC | GCCATTATGC | CAATAGGTGT  |  |
| 1351 | GAATCAGGGG  | ATAACGCAGG | AAAGAACATG | TGAGCAAAAG | GCCACCAAAA  |  |
|      | CTTAGTCCCC  | TATTGCGTCC | TTTCTTGTAC | AUTCCTTTTC | CGGTCCCTTTT |  |
| 1401 | GGCCAGGAAC  | CGTAAAAAGC | CCGCGTTGCT | GGCGTTTTTC | CATAGGCTCC  |  |
|      | CGGCTCCTTG  | GCATTTTTTC | GGCGCAACCA | CGGCAAAAG  | GTATCCGAGG  |  |
| 1451 | GCCCCCCTGA  | CGAGCATCAC | AAAATCGAC  | GCTCAAGTCA | GAGGTCCCGA  |  |
|      | CGGGCGGACT  | GCTCGTAGTG | TTTTTAGCTG | CGAGTTCAGT | CTCCACCCCT  |  |
| 1501 | AACCCGACAG  | GACTATAAAG | ATACCAGGCG | TTTCCCCCTG | GAAGCTCCCT  |  |
|      | TTGGGCTGTC  | CTGATATTTT | TATGGTCCGC | AAAGGGGGAC | CTTCGAGGGA  |  |
| 1551 | CGTGGGCTCT  | CCTTTTCGGA | CCCTGCCGCT | TACCGCATAC | CTGTCCGCTT  |  |
|      | GCACGCGAGA  | GGACAAGGCT | GGGACCCCGA | ATGGCCTATG | GACAGGCGGA  |  |
| 1601 | TTCTCCCTTC  | GGGAAGCGTG | GCGCTTTCTC | ATAGCTCAGC | CTGTAGGTAT  |  |
|      | AAGAGGGAAC  | CCCTTCGCAC | CGCGAAAGAG | TATCGAGTGC | CACATCCATA  |  |
| 1651 | CTCAGTTCTG  | TGTAGGTCGT | TEGETGCAAG | CTGGGCTGTG | TGCACGAACC  |  |
|      | GAGTCAAGCC  | ACATCCAGCA | ACCGAGGTTT | CACCCGACAC | ACGTGCTTGG  |  |
| 1701 | CCGCGTTTCA  | CCCGACCGCT | GCGCCTTATC | CGGTAACAT  | CGTCTTGACT  |  |
|      | GGGGCAAGTC  | GGGCTGGCGA | CGCGGAATAG | GCCATTGATA | GCAGAACTCA  |  |
| 1751 | CAAACCCGGT  | AAGACACGAC | TTATCGCCAC | TGGCAGCAGC | CACTGGTAAC  |  |
|      | GGTTGGGCCA  | TTCTGTGCTG | AATAGCGGTG | ACCGTCTGTC | GTGACCATTG  |  |
| 1801 | AGGATTAGCA  | GAGCGAGGTA | TGTAGGCGGT | GCTACAGAGT | TCTTGAAGTG  |  |
|      | TCCTAATCGT  | CTCGCTCCAT | ACATCCGCCA | CGATGTCTCA | AGAACTTCAC  |  |
| 1851 | GTGGCCTAAC  | TACCGCTACA | CTAGAAGGAC | AGTATTTGGT | ATCTCCGCTC  |  |
|      | CACCGCATTG  | ATGCCGATGT | GATCTTCTCT | TCAATAACCA | TAGACCGGAG  |  |
| 1901 | TGCTGAAGUC  | AGTTACCTTC | GGAAAAAGAC | TTGGTAGCTC | TTGATCCGGC  |  |
|      | ACGACTTCTG  | TCAATGGAAG | CCTTTTCTCT | AACCATCGAG | AACTAGGCCG  |  |
| 1951 | AAACAAACCA  | CGGCTGGTAG | CGGTGGTTTT | TTGTTTGCA  | AGCAGCAGAT  |  |
|      | TTTGTTTGCT  | GGCGACCATC | GCCACCAAAA | APACAAACGT | TCGTGCTCTA  |  |
| 2001 | TACGCGCAGA  | AAAAAAGGAT | CTCAAGABGA | TCCTTTGATC | TTTTCTACGG  |  |
|      | ATGCGCGTCT  | TTTTTTCCTA | GAGTTCTTCT | AGGAAACTAG | AAAAGATGCC  |  |
| 2051 | GGTCTGACGC  | TCAGTGGAAC | GAAAACCTAC | GTTAAGGGAT | TTTGGTCATG  |  |
|      | CCAGACTGUG  | AGTCACCTTG | CTTTTGAGTG | CAATTCCCTA | AAACCAGTAC  |  |
| 2101 | AGATTATCAA  | AAAGGATCTT | CACCTAGATC | CTTTTAAATT | AAAAATGAAG  |  |
|      | TCTAATAGTT  | TTTCCTAGAA | GTGGATCTAG | GAAAAATTAA | TTTTTACTTC  |  |

14/14

pMOD (Cm)

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2151 TTTTAAATCA ATCTAAAGTA TATATGAGTA AACTTCCTCT GACAGTTACC
    AAAATTTAGT TAGATTTTAT ATATACTCAT TTGAACCAGA CTGTCAATGG
2201 AATGCTTAAT CAGTGAGGCA CTTATCTCAG CGATCTCTCT ATTTCTTTCA
    TTACGAATTA GTCACTCGGT GCATAGAGTC GCTAGACAGA TAAAGCAAGT
2251 TCCATAGTTG CCTGACTCCC CCTCGTGTAG ATAACTACGA TACCGGAGGG
    AGGTATCAAC GGAAGGAGGG GCACACATC TATTGATGCT ATGCCCTCCC
2301 CTTACCATCT GGUUCCAGTG CTGCAATGAT ACCGCCAGAC CCAGGCTCAC
    GAATGGTAGA CCGGGGTCAG GACGTTACTA TGGCGCTCTG GGTGCGAGTG
2351 CCGCTCCAGA TTTATCAGCA ATAAACCAAC CAGCCGGAAG GCGCGAGGCG
    GCGGAGGTCT AAATAGTCGT TATTTGGTCC CTCGGCCTTC CCGGCTCCCG
2401 AGAAGTGGTC CTGCAACTTT ATCCGCTCTC ATCCAGTCTA TTAATTCTTG
    TCTTCACCAAG GACGTTGAAA TAGGGCGGAGG TAGGTCAGAT AATTAAACAAC
2451 CCGGGAAGCT AGACTAAGTA GTTCCGCCAGT TAATAGTTTG CGCAACGTTG
    GGCCCTTCGA TCTCATTCAT CAAGCGCTCA ATTATCAAAC GCGTTCCAAC
2501 TTGCCATTGC TACAGGCATC GTCGTGTAC GCTCGTCGT TGGTATGGCT
    AACGGTAACG ATGTCCGTAG CACCACAGTG CGAGCAGCAA ACCATACCGA
2551 TCATTCAGCT CCGGTTCCCA ACGATCAAGG CGAGTTACAT GATCCCCCAT
    AGTAAGTCGA GGCCAAGGGT TGCTAGTTCC GCTCAATGTA CTAGGGGGTA
2601 GTTGTGCAAA AAGCGGGTTA GCTCCTTCGG TCCTCCGATC GTTGTGAGAA
    CAACACGTTT TTTCGCCAAT CGAGGAACCC AGGAGGCTAC CAACAGTCTT
2651 GTAAGTTGGC CGCAGTGTTA TCACTCATGG TTATGGCACC ACTGCATAAT
    CATTTCAACCG GCCTCACAAT AGTGAGTACC AATACCGTCC TGACGTATTA
2701 TCTCTTACTG TCATGCCATC CGTAAGATGC TTTCTGTGA CTGGTGAGTA
    AGAGAATGAC AGTACGGTAG GCATTCTACG AAAAGACACT GACCACTCAT
2751 CTCAACCAAG TCATTCTGAC AATAGTGTAT GCGGCCACCG AGTTGCTCTT
    GAGTTGGTTC AGTAAGACTC TTATCACATA CGCCGCTGGC TCAACGAGAA
2801 GCGGCGCGTC AATACGGGAT AATACCGGCG CACATAGCAG AACTTTAAAA
    CGGGCGCGCAG TTATGCCCTA TTATGCGGCG GTGTATCGTC TTGAAATTTT
2851 GTGCTCATCA TTGGAAAACG TTCCTCGGGG CGAAAACCTCT CAAGGATCTT
    CACGAGTAGT AACCTTTTGC AAGAAGCCCC GCTTTTGAGA GTTCTTAGAA
    ~~~~~~
 ApaLI
    ~~~~~~
2901 ACCGCTGTTG AGATCCAGTT CGATGTAACC CACTCGTGCA CCCAACTGAT
    TGGCGACAAC TCTAGGTCAA GCTACATTTG GTGAGCACGT GGGTTGACTA
2951 CTTCAGCATC TTTTACTTTC ACCAGCGTTT CTGGGTGAGC AAAAACAGGA
    CAAGTCGTAG AAAATGAAAG TGGTCGCAAA GAUCCACTCG TTTTGTCTCT
3001 AGGCAAAATG CCGCAAAAAA GGGAAATACC GCGACACGGA AATGTTGAAT
    TCCGTTTTAC GCGGTTTTTT CCCTTATTCC CGCTGTGCCT TTACAACCTA
3051 ACTCATACTC TTCCTTTTTT AATATTATTG AAGCATTTAT CAGGGTTATT
    TGAGTATGAG AAGGAAAAAG TTATAATAAC TTCGTAAATA GTCCCAATAA
3101 GTCTCATGAG CGGATACATA TTTGAATGTA TTTAGAAAAA TAAACAAATA
    CAGAGTACTC GCCTATGTAT AAACCTACAT AAATCTTTTT ATTTGTTTAT
3151 GGGGTTCCGC GCACATTTCC CCGAAAAGTG CCACCTGACG TCTAACAAAC
    CCCCAGGGCG CGTGTAAAGG GGCTTTTTCAC GGTGGACTGC AGATTCTTTC
3201 CATTATTATC ATGACATTAA CCTATAAAAA TAGGCGTATC ACGAG
    GTAATAATAG TACTGTAATT GGATATTTTT ATCCGCATAG TGCTC

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